

DSP-3, encoded by 501 base pairs

```

1  CCGCGCGCGGT GCTCCGCGCT GTACCATGCC ATAGTGGCGC TCGGACCCCA CGGCGCGCGGC
61  GGTAGCGCTTC GCTTCAGCC ACCGCGCGGA ATGGGATGAA CAGATCCTG CCGCGCGCTGT
121 ACCTCGGCAA CTTCAAGAT GCGAGAGAG CGGAACAATT GAGCAAGAAC AAGGTGACAC
181 ATATCTGTTC TGTCCAGAT AGTCCAGGC TATGTTGGAG GACAAGACAT TTCAAAGAAA
241 GTATTAAATT CATTACAGAG TCGCGCGCTC GCGGTGAGAG CTGCGCTGTA CACTGCGCTGG
301 CCGCGCGCTC CAGGAGCGTG ACGCTCGCTG TCGCATACAT CATGACCGTC ACTGACTTTG
361 GCTGGGAGGA TCGCGTGCAC ACCGCTCGTG CCGGGAGATC CTGTGCCAAC CCGAAGGTGG
421 GCTTCCAGAG ACAGCTCCAG GAGTTTACAG ACCATGAGGT CCATCAGTAT CCGCAGTGGC
481 TGAAGGAGCA ATATGGAGAG AGCGCTTTGC AGGATCCAGA AGRAGCCAAA AACATTCCTG
541 CCGGTCAGAG AATTCCTGAG TTCTGGGCTT TTCTCAGAAG ACTGTATGT ACTGTAGTT
601 TGTGAANTAT TGCAAAACCCG CAGAGTTTAG GCTGTGCTG CCAAAAAGAA AAGCAACATA
661 GAGTTTAAGT ATCCAGTAGT GATTGTAAA CTGTGTTTC ATTTGAAGCT GAATATATAC
721 GTAGTCATGT TTATGTTGAG AACTAAGGAT ATTCTTTAGC AAGAGAAAT ATTTTCCCTT
781 TATCCCCACT GCTGTGGAGG TTCTGTACC TCGCTTGAT GCTGTAAAG ATCCCGGAG
841 CCTTGGCGCA CTGCGTTGTG GGTGCTTGG CGCTC

```

FIG.1

009040" 0254450

FIG.2

Translated, 167 amino acids

MGNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSPLGCWRTRHFKESEIKFIHECRLRGESCLVHCLA
GVSRSVTLVIA YIMTVTDFGWEDALHTVRAGRSCANPNVGFQRQLQEFKHEVHQYRQWLKEEYGESPLQD
AEEAKNILAAPGILKFWAFLRRL*

1 10 20 30 40 50 60 70 80 90 100
 PYS11, SOLURO-PNSHIPSOSP1 SNGSPSE PVEI IPI YI GIGKDSIHL DVI EEFQIKYII NVIPNI PAI FENGGEFKYQIPI SDHUSONI SUFFPENTSEID
 MKP-7, IMKELPSSNIESHSGSPVPSOPPI PVQII IPI YI GIGKDSIHL DVI GKGKII NVIPNI PAI FENGGEFKYQIPI SDHUSONI SUFFPENTSEID
 PACTI PPHGHEMSHSHRPPI YONGPVEI IPI YI GIGKDSIHL DVI GKGKII NVIPNI PAI FENGGEFKYQIPI SDHUSONI SUFFPENTSEID
 MKP-1, PI STIVPDSHSGSPVPSOPPI PVQII IPI YI GIGKDSIHL DVI GKGKII NVIPNI PAI FENGGEFKYQIPI SDHUSONI SUFFPENTSEID
 MKP-4, PVPSNIEPIHL GCSSEGIPLNOGGPVEI IPI YI GIGKDSIHL DVI GKGKII NVIPNI PAI FENGGEFKYQIPI SDHUSONI SUFFPENTSEID
 MKP-5, SERHILISQIKPYVNVSYRPHVNOGGPVEI IPI YI GIGKDSIHL DVI GKGKII NVIPNI PAI FENGGEFKYQIPI SDHUSONI SUFFPENTSEID
 NVHS
 MSP-3
 Consensus
 VPSVGI IRII PDI YI GIGKDSIHL DVI GKGKII NVIPNI PAI FENGGEFKYQIPI SDHUSONI SUFFPENTSEID
 MONGHMKIPI PDI YI GIGKDSIHL DVI GKGKII NVIPNI PAI FENGGEFKYQIPI SDHUSONI SUFFPENTSEID
 GPV IIP IYIGS KDA 2 \$ GIL INVS S P UK IP D S f eal FID

101 110 120 130 140 150 160 171
 PYS11, EARGKUCGY VHG1 AGISRSVIVVNY MKI M SMHNYUEYKHKSHD SPHTHNGOI I OFERTI GI SS
 MKP-7, EARGKUCGY VHG1 AGISRSVIVVNY MKI M SMHNYUEYKHKSHD SPHTHNGOI I OFERTI GI SS
 PACTI SYKMGKGY VHG1 AGISRSVIVVNY MKI M SMHNYUEYKHKSHD SPHTHNGOI I OFERTI GI SS
 MKP-1, SEKHNGGY VHG1 AGISRSVIVVNY MKI M SMHNYUEYKHKSHD SPHTHNGOI I OFERTI GI SS
 MKP-4, NVKIM KGY VHG1 AGISRSVIVVNY MKI M SMHNYUEYKHKSHD SPHTHNGOI I OFERTI GI SS
 MKP-5, CVRI KGY VHG1 AGISRSVIVVNY MKI M SMHNYUEYKHKSHD SPHTHNGOI I OFERTI GI SS
 NVHS
 MSP-3
 Consensus
 EARGKUCGY VHG1 AGISRSVIVVNY MKI M SMHNYUEYKHKSHD SPHTHNGOI I OFERTI GI SS
 PACTI SYKMGKGY VHG1 AGISRSVIVVNY MKI M SMHNYUEYKHKSHD SPHTHNGOI I OFERTI GI SS

FIG.3

DSP-3

Northern blot analysis

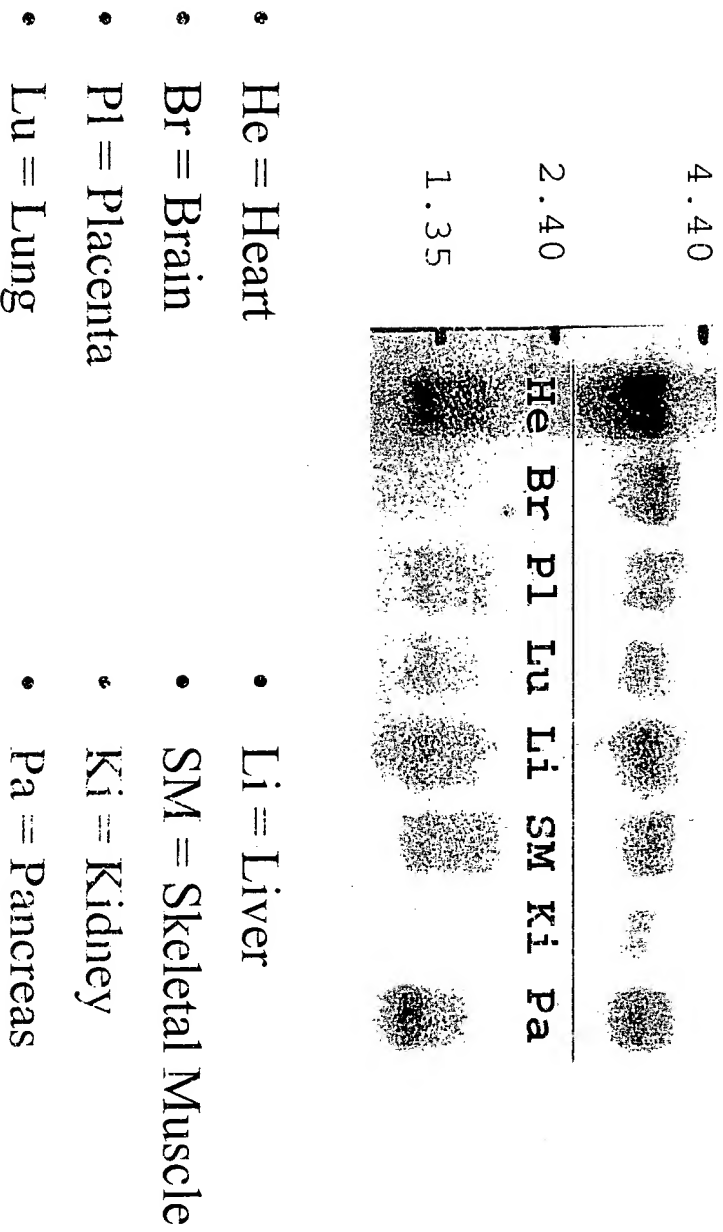


FIGURE 4

09544525.040000